

SEQUENCE LISTING

<110> Seeley, Todd W.

4120 · *nuBUB3* GENE INVOLVED IN HUMAN CANCERS

130 - PP-01406.004/200130.438D1

(140) 13

(141 · 2002-02-27)

(160) 32

(1/0 · FastSEQ for Windows Version 4.0)

210 · 1

1211 - 2619

### mtDNA

### 113. *Homo sapien*

1400

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tgtccattt agttgaccag ccgttggta tttaaagttaa aagaaaaaa attatagtga	1930
gaatqagatt catttcaatg taatgacta aagcagaaca cgaacttagt ttggcattt	2040
ctagtttagtt ccaaatagta ttttgttgt caaactttaa aatttataatt aatttgc当地	2150
tgtatgttcc tgaatggac tttttttttt cttgagattt attttatccg tgatgttattt	2160
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tgtttttttt ctgaaaccat tttttgaaat gtattttttt ctttgcagttt ccaccaatc	2280
atccatgtgaa agtgggtttt tttttttttt tttttttttt tttttttttt tttttttttt	2340
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&lt;210&gt; 2

&lt;211&gt; 323

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 2

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Ser Ser Thr Asp Thr Ser Val Arg Leu Tyr Asp Val Pro Ala Asn Ser	
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Met Arg Leu Lys Tyr Gln His Thr Gly Ala Val Leu Asp Cys Ala Phe	
50 55 60	
Tyr Asp Pro Thr His Ala Trp Ser Gly Gly Leu Asp His Gln Leu Lys	
65 70 75 80	
Met His Asp Leu Asn Thr Asp Gln Glu Asn Leu Val Gly Thr His Asp	
85 90 95	
Ala Pro Ile Arg Cys Val Gln Tyr Cys Pro Glu Val Asn Val Met Val	
100 105 110	
Thr Gly Ser Trp Asp Gln Thr Val Lys Leu Trp Asp Pro Arg Thr Pro	
115 120 125	
Cys Asn Ala Gly Thr Phe Ser Gln Pro Glu Lys Val Tyr Thr Leu Ser	
130 135 140	
Val Ser Gly Asp Arg Leu Ile Val Gly Thr Ala Arg Arg Val Leu	
145 150 155 160	
Val Trp Asp Leu Arg Asn Met Gly Tyr Val Gln Gln Arg Arg Glu Ser	
165 170 175	
Ser Leu Lys Tyr Gln Thr Arg Cys Ile Arg Ala Phe Pro Asn Lys Gln	
180 185 190	
Gly Tyr Val Leu Ser Ser Ile Gln Gly Arg Val Ala Val Glu Tyr Leu	
195 200 205	
Asp Pro Ser Pro Glu Val Gln Lys Lys Tyr Ala Phe Lys Cys His	
210 215 220	
Arg Leu Lys Glu Asn Asn Ile Gln Gln Ile Tyr Pro Val Asn Ala Ile	
225 230 235 240	
Ser Phe His Asn Ile His Asn Thr Phe Ala Thr Gly Gly Ser Asp Gly	
245 250 255	
Phe Val Asn Ile Trp Asp Pro Phe Asn Lys Lys Arg Leu Cys Gln Phe	
260 265 270	

2210 • 5

11111 - 3441

### 1.12. DNA

### 113. *Homo sapien*

1400 3

• 210 - 4  
• 211 - 1986  
• 212 - PRT  
• 213 - *Homo sapiens*

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 Trp Val Glu Glu Asn Phe Pro Gln Asn Lys Glu Tyr Leu Ile Thr Leu  
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 50 55 60  
 Asp Pro Arg Phe Ile Ser Tyr Cys Leu Lys Phe Ala Glu Tyr Asn Ser  
 65 70 75 80  
 Asp Leu His Gln Phe Phe Glu Phe Leu Tyr Asn His Gly Ile Gly Thr  
 85 90 95  
 Leu Ile Ser Pro Leu Tyr Ile Ala Trp Ala Gly His Leu Glu Ala Gln  
 100 105 110  
 Gly Gln Leu Gln His Ala Ser Ala Val Leu Gln Arg Gly Ile Gln Asn  
 115 120 125  
 Gln Ala Glu Pro Arg Glu Phe Leu Gln Gln Gln Tyr Arg Leu Phe Gln  
 130 135 140  
 Thr Arg Leu Thr Gln Thr His Leu Pro Ala Gln Ala Arg Thr Ser Glu  
 145 150 155 160  
 Pro Leu His Asn Val Gln Val Leu Asn Gln Met Ile Thr Ser Lys Ser  
 165 170 175  
 Asn Pro Gly Asn Asn Met Ala Cys Ile Ser Lys Asn Gln Gly Ser Glu  
 180 185 190  
 Leu Ser Gly Val Ile Ser Ser Ala Cys Asp Lys Glu Ser Asn Met Glu  
 195 200 205  
 Arg Arg Val Ile Thr Ile Ser Lys Ser Glu Tyr Ser Val His Ser Ser  
 210 215 220

Leu Ala Ser Lys Val Asp Val Glu Gln Val Val Met Tyr Cys Lys Glu  
 225 230 235 240  
 Lys Leu Ile Arg Gly Glu Ser Glu Phe Ser Phe Glu Glu Leu Arg Ala  
 245 250 255  
 Gln Lys Tyr Asn Gln Arg Arg Lys His Gln Trp Val Asn Glu Asp  
 260 265 270  
 Arg His Tyr Met Lys Arg Lys Gln Ala Asn Ala Phe Glu Glu Leu  
 275 280 285  
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 325 330 335  
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 370 375 380  
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 385 390 395 400  
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 405 410 415  
 Pro Gln Ser Gly Ala Glu Ile Lys Glu Gly Cys Glu Thr His Lys Val  
 420 425 430  
 Ala Asn Thr Ser Ser Phe His Thr Thr Pro Asn Thr Ser Leu Gly Met  
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 Gln Asp Ala Phe Glu Ala Gln Phe Gln Lys Asn Val Arg Ser Ser Gly  
 500 505 510  
 Ala Trp Gly Val Asn Lys Ile Ile Ser Ser Leu Ser Ser Ala Phe His  
 515 520 525  
 Val Phe Glu Asp Gly Asn Lys Glu Asn Tyr Gly Leu Pro Gln Pro Lys  
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 Asn Lys Pro Thr Gly Ala Arg Thr Phe Gly Glu Arg Ser Val Ser Arg  
 545 550 555 560  
 Leu Pro Ser Lys Pro Lys Gln Glu Val Pro His Ala Glu Glu Phe Leu  
 565 570 575  
 Asp Asp Ser Thr Val Trp Gly Ile Arg Cys Asn Lys Thr Leu Ala Pro  
 580 585 590  
 Ser Pro Lys Ser Pro Gly Asp Phe Thr Ser Ala Ala Gln Leu Ala Ser  
 595 600 605  
 Thr Pro Phe His Lys Leu Pro Val Glu Ser Val His Ile Leu Glu Asp  
 610 615 620  
 Lys Glu Asn Val Val Ala Lys Gln Cys Thr Gln Ala Thr Leu Asp Ser  
 625 630 635 640  
 Cys Glu Glu Asn Met Val Val Pro Ser Arg Asp Gly Lys Phe Ser Pro  
 645 650 655

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 Ala Ser Leu Leu Arg Leu Ser Gln Pro Ala Ala Gly Gly Val Leu Thr  
 675 680 685  
 Cys Glu Ala Gln Leu Gly Val Gln Ala Cys Arg Leu Thr Asp Thr Asp  
 690 695 700  
 Ala Ala Ile Ala Glu Asp Pro Pro Asp Ala Ile Ala Gly Leu Gln Ala  
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 Gln Trp Met Gln Met Ser Ser Leu Gly Thr Val Asp Ala Pro Asn Phe  
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 Ile Val Gly Asn Pro Trp Asp Asp Lys Leu Ile Phe Lys Leu Leu Ser  
 740 745 750  
 Gly Leu Ser Lys Pro Val Ser Ser Tyr Pro Asn Thr Phe Glu Trp Gln  
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 Cys Lys Leu Pro Ala Ile Lys Pro Lys Thr Gln Phe Gln Leu Gly Ser  
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 785 790 795 800  
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 Lys Phe Val Leu Lys Val Gln Lys Pro Ala Asn Pro Trp Glu Phe Tyr  
 820 825 830  
 Ile Gly Tyr Gln Leu Met Gln Arg Leu Lys Pro Ser Met Gln His Met  
 835 840 845  
 Phe Met Lys Phe Tyr Ser Ala His Leu Phe Gln Asn Gln Ser Val Leu  
 850 855 860  
 Val Gly Glu Leu Tyr Ser Tyr Gln Leu Leu Asn Ala Ile Asn Leu  
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 885 890 895  
 Phe Ala Met Arg Met Leu Tyr Met Ile Gln Gln Val His Asp Cys Gln  
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 Ile Ile His Gln Asp Ile Lys Pro Asp Asn Phe Ile Leu Gln Asn Gln  
 915 920 925  
 Phe Leu Gln Gln Asp Asp Gln Asp Asp Leu Ser Ala Gln Leu Ala Leu  
 930 935 940  
 Ile Asp Leu Gln Gln Ser Ile Asp Met Lys Leu Phe Pro Lys Gly Thr  
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 965 970 975  
 Leu Ser Asn Lys Pro Trp Asn Tyr Gln Ile Asp Tyr Phe Gln Val Ala  
 980 985 990  
 Ala Thr Val Tyr Cys Met Leu Phe Gln Thr Tyr Met Lys Val Lys Asn  
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 Cys His His Leu Pro Ser Leu Asp Leu Leu Arg Gln Lys Leu Lys Lys  
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His Arg Tyr Pro Thr Ser Ile Ala Ser Leu Ala Phe Ser Asn Asp Gly		
275	280	285
Thr Thr Leu Ala Ile Ala Ser Ser Tyr Met Tyr Glu Met Asp Asp Thr		
290	295	300
Glu His Pro Glu Asp Gly Ile Phe Ile Arg Gln Val Thr Asp Ala Glu		
315	310	315
Thr Lys Pro Lys Val His Leu Ile Ile Leu		
325	330	

4.110> 28

4.111> 341

4.112> PRT

4.113> *Saccharomyces cerevisiae*

4.110> 28

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Gly Ser Leu Thr Val Tyr Lys Phe Asp Ile Gln Ala Lys Asn Val Asp			
35	40	45	
Ile Leu Gln Ser Leu Arg Tyr Lys His Pro Leu Leu Cys Cys Asn Phe			
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100	105	110	
Asp Lys Leu Ile Ala Ala Ser Trp Asp Gly Leu Ile Glu Val Ile Asp			
115	120	125	
Pro Arg Asn Tyr Gly Asp Gly Val Ile Ala Val Lys Asn Leu Asn Ser			
130	135	140	
Asn Asn Thr Lys Val Lys Asn Lys Ile Phe Thr Met Asp Thr Asn Ser			
145	150	160	
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Tyr Ala Cys Ser Ser Ile Asp Gly Arg Val Ala Val Glu Phe Phe Asp			
210	215	220	
Asp Gln Gly Asp Asp Tyr Asn Ser Ser Lys Arg Phe Ala Phe Arg Cys			
225	230	235	240
His Arg Leu Asn Leu Lys Asp Thr Asn Leu Ala Tyr Pro Val Asn Ser			
245	250	255	
Ile Glu Phe Ser Pro Arg His Lys Phe Leu Tyr Thr Ala Gly Ser Asp			
260	265	270	
Gly Ile Ile Ser Cys Trp Asn Leu Gln Thr Arg Lys Lys Ile Lys Asn			
275	280	285	

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 Asn Ile Leu Cys Leu Ala Thr Ser Asp Asp Thr Phe Lys Thr Asn Ala  
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 Ala Ile Asp Gln Thr Ile Glu Leu Asn Ala Ser Ser Ile Tyr Ile  
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 Phe Asp Tyr Glu Asn  
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3210 . . 9  
 3211 . . 26  
 3212 . . PRT  
 3213 . . Mus musculus

3200 . . 9  
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 Ser Ser Itp Asp Thr Ser Val Arg Leu Tyr Asp Val Pro Ala Asn Ser  
 35 40 45  
 Met Asn Leu Lys Tyr Gln His Thr Gly Ala Val Leu Asp Cys Ala Phe  
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 Tyr Asp Pro Thr His Ala Trp Ser Gly Leu Asp His Gln Leu Lys  
 65 70 75 80  
 Ilet His Asp Leu Asn Thr Asp Gln Glu Asn Leu Val Gly Thr His Asp  
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 Ala Trp Ile Arg Cys Val Glu Tyr Cys Pro Glu Val Asn Val Met Val  
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 Thr Gly Ser Trp Asp Gln Thr Val Lys Leu Trp Asp Pro Arg Thr Pro  
 115 120 125  
 Lys Asn Ala Gly Thr Phe Ser Gln Pro Glu Lys Val Tyr Thr Leu Ser  
 130 135 140  
 Val Ser Gly Asp Arg Leu Ile Val Gly Thr Ala Gly Arg Arg Val Leu  
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 Ser Leu Lys Tyr Gln Thr Arg Cys Ile Arg Ala Phe Pro Asn Lys Gln  
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 Gly Tyr Val Leu Ser Ser Ile Glu Gly Arg Val Ala Val Glu Tyr Leu  
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 Arg Leu Lys Glu Asn Asn Ile Glu Gln Ile Tyr Pro Val Asn Ala Ile  
 225 230 235 240  
 Ser Phe His Asn Ile His Asn Thr Phe Ala Thr Gly Gly Ser Asp Gly  
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 Phe Val Asn Ile Trp Asp Pro Phe Asn Lys Lys Arg Leu Cys Gin Phe  
 260 265 270  
 His Arg Tyr Pro Thr Ser Ile Ala Ser Leu Ala Phe Ser Asn Asp Gly  
 275 280 285  
 Thr Thr Leu Ala Ile Ala Ser Ser Tyr Met Tyr Glu Met Asp Asp Thr  
 290 295 300  
 Glu His Pro Glu Asp Gly Ile Phe Ile Arg Gln Val Thr Asp Ala Gln

305	310	315	320
Thr Lys Pro Lys Ser Thr			
325			
330: 30			
331: 368			
332: PRT			
333: Homo sapien			
340: 30			
Met Ser Leu Phe Gly Thr Thr Ser Gly Phe Gly Thr Ser Gly Thr Ser			
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Glu Val Thr Ser Ser Pro Asp Asp Ser Ile Gly Cys Leu Ser Phe Ser			
35 40 45			
Pro Pro Thr Leu Pro Gly Asn Phe Leu Ile Ala Gly Ser Trp Ala Asn			
50 55 60			
Asp Val Arg Cys Trp Glu Val Gln Asp Ser Gly Gln Thr Ile Pro Lys			
65 70 75 80			
Ala Gln Gln Met His Thr Gly Pro Val Leu Asp Val Cys Trp Ser Asp			
85 90 95			
Asp Gly Ser Lys Val Phe Thr Ala Ser Cys Asp Lys Thr Ala Lys Met			
100 105 110			
Trp Asp Leu Ser Ser Asn Glu Ala Ile Gln Ile Ala Gln His Asp Ala			
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130 135 140			
Met Thr Gly Ser Trp Asp Lys Thr Leu Lys Phe Trp Asp Thr Arg Ser			
145 150 155 160			
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210 215 220			
Gln Asn Lys Pro Thr Gly Phe Ala Leu Gly Ser Ile Glu Gly Arg Val			
225 230 235 240			
Ala Ile His Tyr Ile Asn Pro Pro Asn Pro Ala Lys Asp Asn Phe Thr			
245 250 255			
Phe Lys Cys His Arg Ser Asn Gly Thr Asn Thr Ser Ala Pro Gln Asp			
260 265 270			
Ile Tyr Ala Val Asn Gly Ile Ala Phe His Pro Val His Gly Thr Leu			
275 280 285			
Ala Thr Val Gly Ser Asp Gly Arg Phe Ser Phe Trp Asp Lys Asp Ala			
290 295 300			
Arg Thr Lys Leu Lys Thr Ser Glu Gln Leu Asp Gln Pro Ile Ser Ala			
305 310 315 320			
Cys Cys Phe Asn His Asn Gly Asn Ile Phe Ala Tyr Ala Ser Ser Tyr			
325 330 335			
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340 345 350			

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<210> 31

<211> 352

<212> PRT

<213> Schizosaccharomyces pombe

<400> 31

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 35 40 45  
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 50 55 60  
 Ser Ile Gly Lys Ala Leu Tyr Glu His Gln Gly Pro Val Leu Ser Val  
 65 70 75 80  
 Asn Trp Ser Arg Asp Gly Thr Lys Val Ala Ser Gly Ser Val Asp Lys  
 85 90 95  
 Ser Ala Lys Val Phe Asp Ile Gln Thr Gly Gln Asn Gln Gln Val Ala  
 100 105 110  
 Ala His Asp Asp Ala Val Arg Cys Val Arg Phe Val Glu Ala Met Gly  
 115 120 125  
 Thr Ser Pro Ile Leu Ala Thr Gly Ser Trp Asp Lys Thr Leu Lys Tyr  
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 Trp Asp Leu Arg Gln Ser Thr Pro Ile Ala Thr Val Ser Leu Pro Glu  
 145 150 155 160  
 Arg Val Tyr Ala Met Asp Cys Val His Pro Leu Leu Thr Val Ala Thr  
 165 170 175  
 Ala Glu Arg Asn Ile Cys Val Ile Asn Leu Ser Glu Pro Thr Lys Ile  
 180 185 190  
 Phe Lys Leu Ala Met Ser Pro Leu Lys Phe Gln Thr Arg Ser Leu Ala  
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 Cys Phe Ile Lys Gly Asp Gly Tyr Ala Ile Gly Ser Val Glu Gly Arg  
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 Cys Ala Ile Gln Asn Ile Asp Glu Lys Asn Ala Ser Gln Asn Phe Ser  
 225 230 235 240  
 Phe Arg Cys His Arg Asn Gln Ala Gly Asn Ser Ala Asp Val Tyr Ser  
 245 250 255  
 Val Asn Ser Ile Ala Phe His Pro Gln Tyr Gly Thr Phe Ser Thr Ala  
 260 265 270  
 Gly Ser Asp Gly Thr Phe Ser Phe Trp Asp Lys Asp Ser His Gln Arg  
 275 280 285  
 Leu Lys Ser Tyr Pro Asn Val Gly Gly Thr Ile Ser Cys Ser Thr Phe  
 290 295 300  
 Asn Arg Thr Gly Asp Ile Phe Ala Tyr Ala Ile Ser Tyr Asp Trp Ser  
 305 310 315 320  
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 325 330 335  
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 340 345 350

<210 · 32  
 <211 · 365  
 <212 · PRT  
 <213 · *Saccharomyces cerevisiae*

<400 · 32  
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 Asp Phe Met Phe Ser Ala Ser Ser Trp Asp Gly Lys Val Arg Ile Trp  
 50 55 60  
 Asp Val Gln Asn Gly Val Pro Gln Gly Arg Ala Gln His Glu Ser Ser  
 65 70 75 80  
 Ser Pro Val Leu Cys Thr Arg Trp Ser Asn Asp Gly Thr Lys Val Ala  
 85 90 95  
 Ser Gly Gly Cys Asp Asn Ala Leu Iys Leu Tyr Asp Ile Ala Ser Gly  
 100 105 110  
 Gln Thr Gln Gln Ile Gly Met His Ser Ala Pro Ile Lys Val Leu Arg  
 115 120 125  
 Phe Val Gln Cys Gly Pro Ser Asn Thr Gln Cys Ile Val Thr Gly Ser  
 130 135 140  
 Trp Asp Iys Thr Ile Lys Tyr Isp Asp Met Arg Gln Pro Gln Pro Val  
 145 150 155 160  
 Ser Thr Val Met Met Pro Gln Arg Val Tyr Ser Met Asp Asn Lys Gln  
 165 170 175  
 Ser Leu Leu Val Val Ala Thr Ala Glu Arg His Ile Ala Ile Ile Asn  
 180 185 190  
 Leu Ala Asn Pro Thr Thr Ile Phe Iys Ala Thr Thr Ser Pro Leu Lys  
 195 200 205  
 Trp Gln Thr Arg Cys Val Ala Cys Tyr Asn Glu Ala Asp Gly Tyr Ala  
 210 215 220  
 Ile Gly Ser Val Glu Gly Arg Cys Ser Ile Arg Tyr Ile Asp Asp Gly  
 225 230 235 240  
 Met Gln Lys Lys Ser Gly Phe Ser Phe Iys Cys His Arg Gln Thr Asn  
 245 250 255 260  
 Pro Asn Arg Ala Pro Gly Ser Asn Gly Gln Ser Leu Val Tyr Pro Val  
 265 270  
 Asn Ser Ile Ala Phe His Pro Leu Tyr Gly Thr Phe Val Thr Ala Gly  
 275 280 285  
 Gly Asp Gly Thr Phe Asn Phe Trp Asp Lys Asn Gln Arg His Arg Leu  
 290 295 300  
 Lys Gly Tyr Pro Thr Leu Gln Ala Ser Ile Pro Val Cys Ser Phe Asn  
 305 310 315 320  
 Arg Asn Gly Ser Val Phe Ala Tyr Ala Leu Ser Tyr Asp Trp His Gln  
 325 330 335  
 Gly His Met Gly Asn Arg Pro Asp Tyr Pro Asn Val Ile Arg Leu His  
 340 345 350  
 Ala Thr Thr Asp Glu Glu Val Lys Glu Lys Lys Lys Arg  
 355 360 365